



ENTERED

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/027,859

DATE: 01/17/2002

TIME: 17:43:31

Input Set : N:\Crf3\RULE60\10027859.raw

Output Set: N:\CRF3\01172002\J027859.raw

48		85		90		95		
49	cag tcc ccg gca gcg atg aga	cag agc ggc acc tcc cag ccc ctg ctg	453					
50	Gln Ser Pro Ala Ala Met Arg	Gln Ser Gly Thr Ser Gln Pro Leu Leu						
51	100	105	110					
52	atc aac atg tac cta cca gat ccc gtc gga gat ggt ctt ttt aag gaa	501						
53	Ile Asn Met Tyr Leu Pro Asp Pro Val Gly Asp Gly Leu Phe Lys Glu							
54	115	120	125					
55	ggg aag agc ccg agc tgg ggg ccg ctg agc cct gcg gta cag aaa ggc	549						
56	Gly Lys Ser Pro Ser Trp Gly Pro Leu Ser Pro Ala Val Gln Lys Gly							
57	135	140	145					
58	agc ggg cag atc cag ttg tgg cag ttt cta ctg gag ctg ctg gca gac	597						
59	Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Leu Ala Asp							
60	150	155	160					
61	cgc gcg aac gcc ggc tgc atc gcg tgg gag ggc ggc cac ggc gag ttc	645						
62	Arg Ala Asn Ala Gly Cys Ile Ala Trp Glu Gly Gly His Gly Glu Phe							
63	165	170	175					
64	aag ctc acc gac ccc gac gag gtg gcg cga cgc tgg ggc gag cgc aag	693						
65	Lys Leu Thr Asp Pro Asp Glu Val Ala Arg Arg Trp Gly Glu Arg Lys							
66	180	185	190					
67	agc aag ccc aat atg aac tac gac aag cta agt cga gca ctg cgc tac	741						
68	Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser Arg Ala Leu Arg Tyr							
69	195	200	205					
70	tac tac gac aaa aac atc atg agc aag gtg cac ggc aag cgc tac gcc	789						
71	Tyr Tyr Asp Lys Asn Ile Met Ser Lys Val His Gly Lys Arg Tyr Ala							
72	215	220	225					
73	tac cgc ttt gac ttc cag ggc ctg gca cag gct tgc cag cca cca ccc	837						
74	Tyr Arg Phe Asp Phe Gln Gly Leu Ala Gln Ala Cys Gln Pro Pro Pro							
75	230	235	240					
76	gcg cac gcc cac gcc gcc gct gcc gcc gcc gca gcg gca gcc gcc gcc	885						
77	Ala His Ala His Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala							
78	245	250	255					
79	cag gat ggc gca ctt tac aag ctc ccg gct ggt ctg gct cca ctg ccc	933						
80	Gln Asp Gly Ala Leu Tyr Lys Leu Pro Ala Gly Leu Ala Pro Leu Pro							
81	260	265	270					
82	ttc ccc ggc ctc tcc aaa ctc aac ctt atg gca gcc tcg gcc ggc gtg	981						
83	Phe Pro Gly Leu Ser Lys Leu Asn Leu Met Ala Ala Ser Ala Gly Val							
84	275	280	285					
85	gcg ccc gct ggc ttc tct tac tgg cct ggt ccc aac gcc acc gcc gct	1029						
86	Ala Pro Ala Gly Phe Ser Tyr Trp Pro Gly Pro Asn Ala Thr Ala Ala							
87	295	300	305					
88	gcc gcc gcc acc gct gcg ctc tac cca acc ccg ggc ttg cag ccc cct	1077						
89	Ala Ala Ala Thr Ala Ala Leu Tyr Pro Thr Pro Gly Leu Gln Pro Pro							
90	310	315	320					
91	ccc ggg ccc ttt ggc gcg gtg gcc gcc gct tcg cac ttg ggg ggt cat	1125						
92	Pro Gly Pro Phe Gly Ala Val Ala Ala Ala Ser His Leu Gly Gly His							
93	325	330	335					
94	tat cac tagacgggac ggccgggtgc agtggggcct ctccacaca gccagtgacc	1181						
95	Tyr His							
96	340							

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97 aatcccatcc tcatacctggg aggagccccg aagatttccc cgacgttcct ttaccacaga 1241  
98 tttcgttgca gcagccgctc ccagcccagg gaagaaagga tgggaagcct ctgaggtcct 1301  
99 ccttgaatac gaggttcca ggctccatt atcatcacc caggaagggt gcatgtgctc 1361  
100 ccactttaat ttttctcttc caagtctcca gattctggaa ctcccgtctt tttttctct 1421  
101 tctcacctgg agcccctgcc ttctcttta tgaccctag tttctgttt tggttttttt 1481  
102 ttttctcttc tctctcctca tttttttct ctcccacgac ctactccaaa cggtagtacc 1541  
103 tcggtagtac ctgaggtct ctcacactcc ccttttcggg atatgagaag catcaaaaac 1601  
104 atctctgctg ttgtccatcc ctatcccaac actctggctt cgctcccttc cataccacac 1661  
105 tctggcccaa ggaccctcgt ctgtatatat tcctttcagc ccattaaag atccaagctt 1721  
106 caaaaaaaaa aaaaaaaaaa aaaaaaaaa a 1752

108 &lt;210&gt; SEQ ID NO: 2

109 &lt;211&gt; LENGTH: 340

110 &lt;212&gt; TYPE: PRT

111 &lt;213&gt; ORGANISM: Rattus norvegicus

112 &lt;400&gt; SEQUENCE: 2

113	Met	Glu	Asp	Pro	Gly	Gly	Ala	Pro	Leu	Gly	Glu	Arg	Val	Pro	Ala	Pro
114	1				5					10					15	
115	His	Pro	Pro	Gln	Pro	His	Pro	Leu	Thr	Ala	His	Ser	Ser	Ser	Thr	Pro
116				20					25						30	
117	Ala	Pro	Gly	Trp	Ala	Gly	Met	Gln	Leu	Gln	Asp	Pro	Leu	Pro	Pro	His
118				35				40						45		
119	His	Thr	Leu	Ala	Ala	Arg	Ser	Arg	Gln	Ala	Leu	Pro	Asp	Pro	Ala	Ala
120			50				55					60				
121	Ser	Thr	Leu	Pro	Cys	His	Pro	Gln	Ser	Pro	Arg	Ala	Gly	Ile	Gly	Thr
122			65			70					75				80	
123	Pro	Ser	Ala	Lys	Leu	Thr	Cys	Pro	Pro	Val	Arg	Ser	Pro	Pro	Ser	Pro
124					85					90					95	
125	Thr	Ala	Gln	Ser	Pro	Ala	Ala	Met	Arg	Gln	Ser	Gly	Thr	Ser	Gln	Pro
126				100					105					110		
127	Leu	Leu	Ile	Asn	Met	Tyr	Leu	Pro	Asp	Pro	Val	Gly	Asp	Gly	Leu	Phe
128			115					120					125			
129	Lys	Glu	Gly	Lys	Ser	Pro	Ser	Trp	Gly	Pro	Leu	Ser	Pro	Ala	Val	Gln
130			130				135					140				
131	Lys	Gly	Ser	Gly	Gln	Ile	Gln	Leu	Trp	Gln	Phe	Leu	Leu	Glu	Leu	Leu
132			145			150					155				160	
133	Ala	Asp	Arg	Ala	Asn	Ala	Gly	Cys	Ile	Ala	Trp	Glu	Gly	Gly	His	Gly
134				165					170						175	
135	Glu	Phe	Lys	Leu	Thr	Asp	Pro	Asp	Glu	Val	Ala	Arg	Arg	Trp	Gly	Glu
136				180					185					190		
137	Arg	Lys	Ser	Lys	Pro	Asn	Met	Asn	Tyr	Asp	Lys	Leu	Ser	Arg	Ala	Leu
138			195				200						205			
139	Arg	Tyr	Tyr	Tyr	Asp	Lys	Asn	Ile	Met	Ser	Lys	Val	His	Gly	Lys	Arg
140			210				215					220				
141	Tyr	Ala	Tyr	Arg	Phe	Asp	Phe	Gln	Gly	Leu	Ala	Gln	Ala	Cys	Gln	Pro
142			225				230				235				240	
143	Pro	Pro	Ala	His	Ala	His	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala
144				245						250					255	
145	Ala	Ala	Gln	Asp	Gly	Ala	Leu	Tyr	Lys	Leu	Pro	Ala	Gly	Leu	Ala	Pro
146				260					265						270	

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```
147      Leu Pro Phe Pro Gly Leu Ser Lys Leu Asn Leu Met Ala Ala Ser Ala
148              275                      280                      285
149      Gly Val Ala Pro Ala Gly Phe Ser Tyr Trp Pro Gly Pro Asn Ala Thr
150              290                      295                      300
151      Ala Ala Ala Ala Ala Thr Ala Ala Leu Tyr Pro Thr Pro Gly Leu Gln
152      305                      310                      315                      320
153      Pro Pro Pro Gly Pro Phe Gly Ala Val Ala Ala Ala Ser His Leu Gly
154              325                      330                      335
155      Gly His Tyr His
156              340
158 <210> SEQ ID NO: 3
159 <211> LENGTH: 11
160 <212> TYPE: DNA
161 <213> ORGANISM: Polyomavirus enhancer
162 <400> SEQUENCE: 3
163      agcaggaagt g                                     11
165 <210> SEQ ID NO: 4
166 <211> LENGTH: 11
167 <212> TYPE: DNA
168 <213> ORGANISM: Homo sapiens
169 <400> SEQUENCE: 4
170      agcaggaagt t                                     11
172 <210> SEQ ID NO: 5
173 <211> LENGTH: 11
174 <212> TYPE: DNA
175 <213> ORGANISM: Mus musculus
176 <400> SEQUENCE: 5
177      agcggggaagt t                                     11
179 <210> SEQ ID NO: 6
180 <211> LENGTH: 11
181 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
183 <400> SEQUENCE: 6
184      gaaaggaaat a                                     11
186 <210> SEQ ID NO: 7
187 <211> LENGTH: 11
188 <212> TYPE: DNA
189 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 7
191      gataggaagt a                                     11
193 <210> SEQ ID NO: 8
194 <211> LENGTH: 11
195 <212> TYPE: DNA
196 <213> ORGANISM: Mus musculus
197 <400> SEQUENCE: 8
198      cccaggaaat g                                     11
200 <210> SEQ ID NO: 9
201 <211> LENGTH: 11
202 <212> TYPE: DNA
```

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Input Set : N:\Crf3\RULE60\10027859.raw

Output Set: N:\CRF3\01172002\J027859.raw

203 <213> ORGANISM: Mus musculus  
204 <400> SEQUENCE: 9  
205 gggaggaaat g 11  
207 <210> SEQ ID NO: 10  
208 <211> LENGTH: 11  
209 <212> TYPE: DNA  
210 <213> ORGANISM: Homo sapiens  
211 <400> SEQUENCE: 10  
212 atacggaaat t 11  
214 <210> SEQ ID NO: 11  
215 <211> LENGTH: 11  
216 <212> TYPE: DNA  
217 <213> ORGANISM: Mus musculus  
218 <400> SEQUENCE: 11  
219 tacaggatat a 11  
221 <210> SEQ ID NO: 12  
222 <211> LENGTH: 11  
223 <212> TYPE: DNA  
224 <213> ORGANISM: Rattus norvegicus  
225 <400> SEQUENCE: 12  
226 ttcaggaaat t 11  
228 <210> SEQ ID NO: 13  
229 <211> LENGTH: 7  
230 <212> TYPE: PRT  
231 <213> ORGANISM: Artificial Sequence  
232 <220> FEATURE:  
233 <221> NAME/KEY: SITE  
234 <222> LOCATION: (1)  
235 <223> OTHER INFORMATION: The amino acid at this position can be isoleucine,  
236 valine, or leucine.  
237 <220> FEATURE:  
238 <221> NAME/KEY: SITE  
239 <222> LOCATION: (2)  
240 <223> OTHER INFORMATION: The amino acid at this position can be glutamine,  
241 tyrosine, or threonine.  
242 <220> FEATURE:  
243 <221> NAME/KEY: SITE  
244 <222> LOCATION: (5)  
245 <223> OTHER INFORMATION: The amino acid at this position can be glutamic  
246 acid or glutamine.  
247 <220> FEATURE:  
248 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
249 <400> SEQUENCE: 13  
W--> 250 Xaa Xaa Leu Trp Xaa Phe Leu  
251 1 5  
253 <210> SEQ ID NO: 14  
254 <211> LENGTH: 7  
255 <212> TYPE: PRT  
256 <213> ORGANISM: Artificial Sequence

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10027859.raw

Output Set: N:\CRF3\01172002\J027859.raw

L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD

L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14